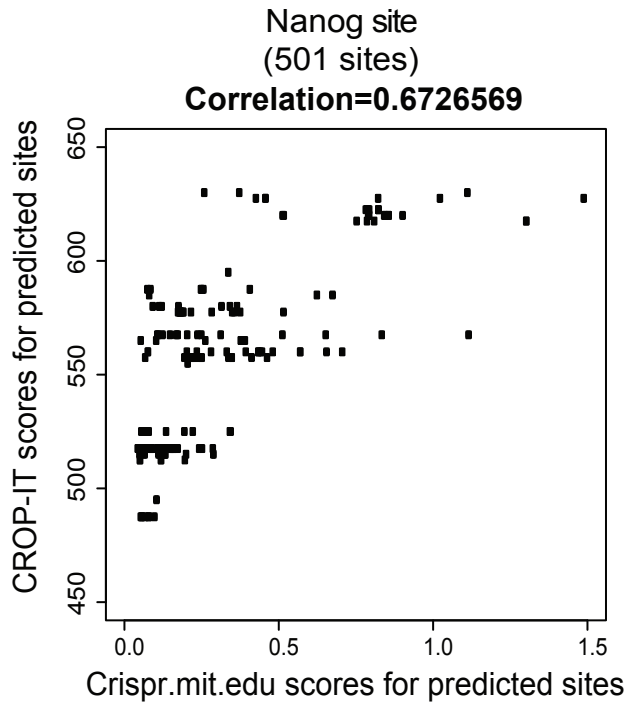
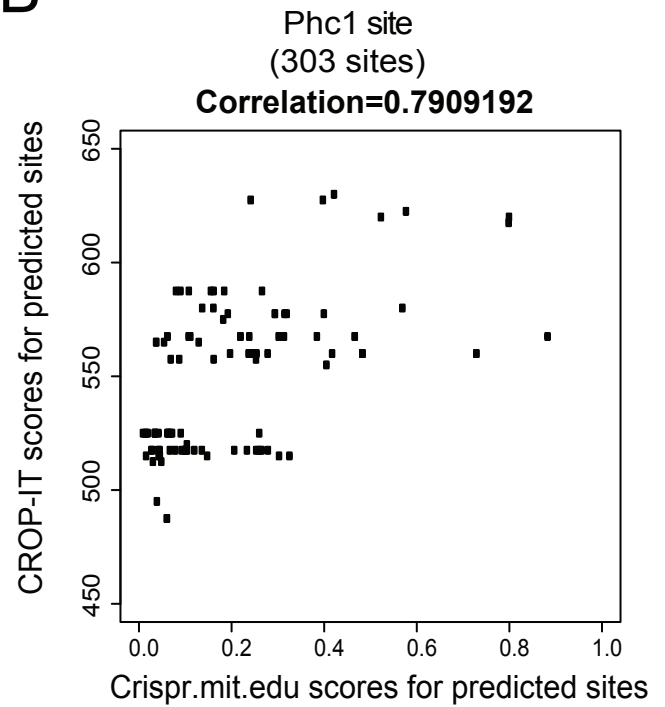


Supplementary Figure 1

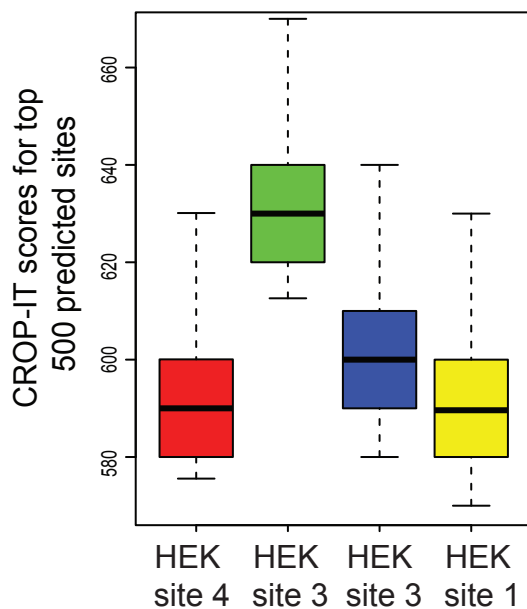
A



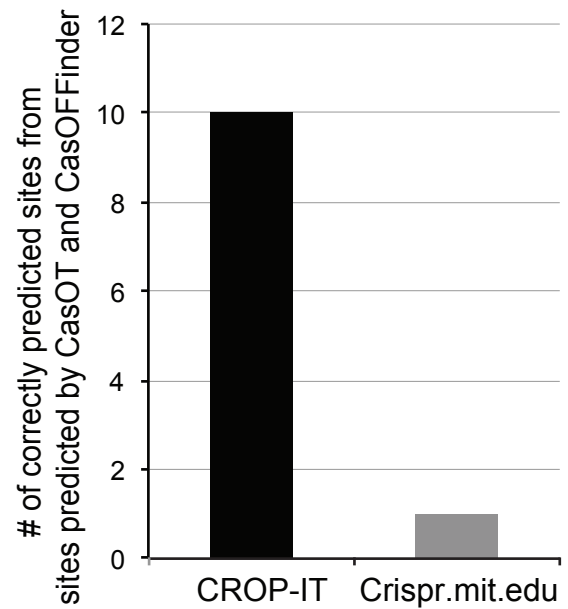
B



C

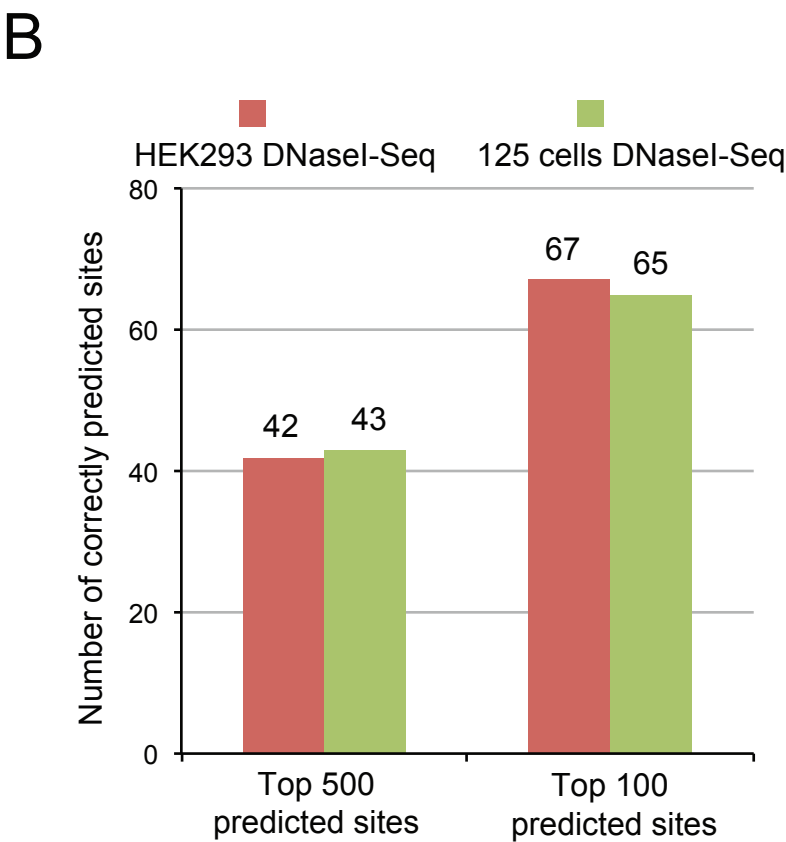
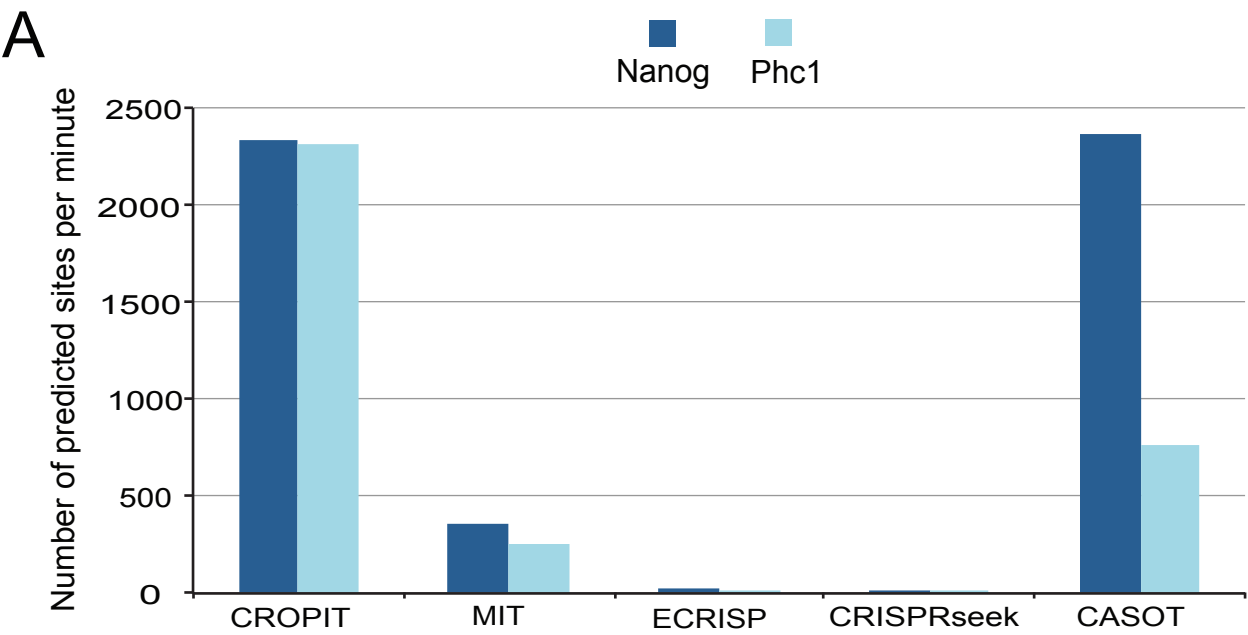


D



Suppl. Fig 1. Comparison of off-target scores predicted by Crispr.mit.edu (X-axis) and CROP-IT (Y-axis) for Nanog **(A)** and PHC1 sgRNAs **(B)**. **(C)** Boxplots of the scores of top 500 predicted sites by CROP-IT for the different sgRNAs used in HEK293T. **(D)** Comparison of performances of CROP-IT and Crispr.mit.edu tool on the overlapping genomic sites predicted by both CasOT tool and CasOFFinder tools.

Supplementary Figure 2



Suppl. Fig 2. (A) Comparative analysis of execution times for different computational tools. Since each tool outputs different number of predicted sites, the comparison has been done based on number of predicted sites per minute (Y-axis) **(B)** Comparison of cell type specific chromatin state data vs aggregate chromatin state of 125 cell types. Number of correctly predicted sites are shown for CROP-IT algorithm with DNase I HS data from HEK 293 cells and aggregate DNase I HS data from 125 different human cell types.